************** [align] **************

options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1

    CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: E1-A0209P-2   498 aa
Sequence 2: E1-A0209P-8   459 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 34
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:   Delayed
Sequence:2   Score:2988
Alignment Score 779

query.aln
CLUSTAL W (1.83) multiple sequence alignment


```
E1-A0209P-2     MATVHQKNMSTLKQRKEDFVTGLNGGSITEINAVTSIALVTYISWNLLKNSNLMPPGISS
E1-A0209P-8     --------MSYKLEKEAFVSNLTGSSSIETGGLLLIGIACNVLWVNMTARNILPKGN-L
                   : *.** **:.*.* *  *  .: *.:.  : *  .  *::* *

E1-A0209P-2     VQYIIDFALNWVALLLSITIYASEPYLLNTLILLPCLLAFIYGKFTSSSKPSNPIYNKKK
E1-A0209P-8     GFLVEFFIFCLIPLFVIYVSSKVGVFTLCIASFLPSFVLHVISPINWDVLRRKPGCCLTK
                 : *: :.*::  .      : *   :**.:: .:. :. ..   :*   .*

E1-A0209P-2     MITQRFQLEKKPYITAYRGGMLILTAIAILAVDFPIFPRRFAKVETWGTSLMDLGVGSFV
E1-A0209P-8     KNENTFDR-RIAGVTFYRSQMMLVTVTCILAVDFTLFPRRYAKVETWGTSLMDLGVGSFM
                 : *:  :. .:* **. *:::*. .******. :**** :*****************:

E1-A0209P-2     FSNGIVSSRALLKNLSLKSKPSFLKNAFNALKSGGTLLFLGLLRLFFVKNLEYQEHVTEY
E1-A0209P-8     FSSGTVAGR--------KNDIKKPNAFKNVLWNSFILLILGFARMFLTKSINYQEHVSEY
                **.* *:.*       *.. :   : *.*..  **:**: *:*:.*.::*****:**

E1-A0209P-2     GVHWNFFITLSLLPLVLTFIDPVTRMVPRCGSIAIFISCIYEWLLLKDDRTLNFLILADRN
E1-A0209P-8     GMHWNFFFTLGFMALGVFFFRRSLKKVSYFNLATFITLLHHCLLVLTP-FQKWALSAPRT
                *:*****:**.::.* : *:     :*. .:* **: ::. **:       :: :* *.

E1-A0209P-2     CFFSANREGIFSFLGYCSIFLWGQNTGFYLLGNKPTLNNLYKPSTQDVVAASKKSSTWDY
E1-A0209P-8     NILAQNREGIASLPGYIAIYFYGMYTGSVVLADRPLMY------------TRAESWKR
                ::: ***** *: ** :*:::* **  :*.::* :        .::.:*.

E1-A0209P-2     WTSVTPLSGLCIWSTIFLVISQLVFQYHPYSVSRRFANLPYTLWVITYNLLFLTGYCLTD
E1-A0209P-8     FQRLLFP--LCILLVLYLVS----NFLSVGVSRRLANTPYVANVAFINMFFLTIYILID
                : :    *** ,.::**    ::. .****:** **. *  *:**** * **.

E1-A0209P-2     KIFGNSSEYY--KVAECLESINSNGLFLFLLANVSTGLVNMSMVTIDSSPLKSFLVLLAY
E1-A0209P-8     AYLFPSSVPYGSRVPKLLEDANNNGLLVFLIANVLTGVVNLSFDTLHSSNAKGLTIMTMY
                : ** *  :*.: **. *.***::**:*** **:**:*: *:.** *: :: *

E1-A0209P-2     GSFIAVISVFLYRKRIFIKL
E1-A0209P-8     LFIICYMAHWLAQHGIRFRL
                :*. :: :* :: * ::*
```


query.dnd
(E1-A0209P-2:0.32789,E1-A0209P-8:0.32789);

```
*************** [align] ***************

options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1

   CLUSTAL W (1.83) Multiple Sequence Alignments


Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: E1-A0209P-2        498 aa
Sequence 2: E1-A0209P-14       598 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  33
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                     Delayed
Sequence:2      Score:3104
Alignment Score 789
```

<u>query.aln</u>
CLUSTAL W (1.83) multiple sequence alignment

```
E1-A0209P-2       MATVHQKNMSTLKQRKEDFVTGLNGGSITEINAVTSIALVTYISWNLLK----------
E1-A0209P-14      ------MGDYKSAKEAFVSDNPGASIWSINAVSLVALATYALWIALSPYIRHGLLNNY
                       *. *. ** **:. *.** .****: :**.** *  *.

E1-A0209P-2       -------------NSNLMPPGISSVQYIIDFALNWVALLLSITIYASEP----------
E1-A0209P-14      LICVLPLLFGVTIFSTSPLVFTSFLSIISLAFITKSQKCFKSVSSPEKPKGQWLDESDSD
                      .  *  ::*. **.:*:  :      :: :.*

E1-A0209P-2       -------------YLLNTLILLPCLLAFIYGKFTSSSKPSNPIY---------------
E1-A0209P-14      EEPAEPASAAGSAAVSPVKLLPSQVAFASGSLLSPDPTTSPMSPSSSSASGHEDPLGIMG
                               :..: ***. :**  *.: *.. .:.*:

E1-A0209P-2       -NKKKMITQRFQLEKK------------------------------PYITAYRGGM
E1-A0209P-14      VNRRRSLLEGVSLDVPSHIDSKVRISPVPYLRLKKSRATKAQWVKEKGRLPFLTVYRAHM
                   *::: : : ..*:                          *::*.**. *

E1-A0209P-2       LILTAIAILAVDFPIFPRRFAKVETWGTSLMDLGVGSFVFSNGIVSSRAL----------
E1-A0209P-14      MLMTVICILAVDFEVFPRWQGKCEDFGTSLMDVGVGSFVFSLGLVSTKSLSPPPPTPTPS
                  ::.*.*.****** :***  .* * :*****:********* *:**::*

E1-A0209P-2       ---LKNLSLKSKPSFLKNAFNALKSGGTLLFLGLLRLFFVKNLEYQEHVTEYGVHWNFFI
E1-A0209P-14      SPALNSHIIPLTPSPFTSILISLRKSIPILVLGFIRLIMVKGSDYPEHVTEYGVHWNFFF
                  *:. : . :** :.. : :*:.. .:*.**:**:**::**. :* **************:

E1-A0209P-2       TLSLLPLVLTFIDPVTRMVPRCGSIAIFISGIYEWLLLKDDRTLNFLILADRNCFFSANRE
E1-A0209P-14      TLALVPVLAVGIRPLTQWLRWSVLGVIISLLHQLWLTYYLQSIVFSFGRSG--IFLANKE
                  **:*:*:*:: .* *:*:   :  . :.:** ::: *   ::: *:  .   :* **:*

E1-A0209P-2       GIFSFLGYCGSIFLWGQNTGFYLLGNKPTLNNLYKPSTQDVVAASKKSSTWDYWTSVTPLS
E1-A0209P-14      GFSSLPGYLSIFLIGLSIGDHVLR-----LSLPPRRERVVSETNEEHEQSHFERKKLDLI
                  *: *: ** **** *. *  ::*      .*   : *  :.::.  .:  *

E1-A0209P-2       GLCIWSTIFLVISQLVFQYHPYSVSRRFANLPYTLWVITYNLLFLTGYCLTDKIFGN--
E1-A0209P-14      MELIGYSLGWWALLGGWIWAGGEVSRRLANAPYVFWVAAYNTTFLLGYLLLTHIIPSPTS
                     *  ::         :  :  .****:** **.:** :** *** **  .  :*:  .

E1-A0209P-2       --SSEYYKVAEGLESINSNGLFLFLLANVSTGLVNMSMVTIDSSPLKSFLVLLAYCSFIA
E1-A0209P-14      SQTSPSILVPPLLDAMNKNGLAIFLAANLLTGLVNVSMKTMYAPAWLSMGVLMLYTLTIS
                   :*   *. *:::*.*** :** **: ****:** *: :..  *: **: *   *:

E1-A0209P-2       VISVFLYRKRIFIKL
E1-A0209P-14      CVGWILKGRRIKI--
                  :. :* :** *
```

<u>query.dnd</u>
(E1-A0209P-2:0.33032,E1-A0209P-14:0.33032);

Appendix B

<pre>
*************** [align] **************

options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1

 CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: E1-A0209P-8   459 aa
Sequence 2: E1-A0209P-14   598 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 33
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:   Delayed
Sequence:2   Score:2939
Alignment Score 741

query.aln
CLUSTAL W (1.83) multiple sequence alignment

E1-A0209P-8   -MSYKLEKEAFVSNLTGSSSIETCGLLLIGIACNVLWVNMTARNILPKGN-----LGFL
E1-A0209P-14   MGDYKSAKEAFVSDNPGASIWSINAVSLVALATYALWIALSPYIRHGLLNNYLICVLPLL
                 .** ******: .*:* , .: *:.:* .**: ::.   *   * :*

E1-A0209P-8   VEFFIFCLIPLFVIYVSSKVGVFTLCIAS----------------------------
E1-A0209P-14   FGVTIFSTSPLVFTSFLSIISLAFITKSQKCFKSVSSPEKPKGQWLDESDSDEEPAEPAS
                . . **. **.. . * :.: : :.

E1-A0209P-8   ---FL
E1-A0209P-14   AAGSAAVSPVKLLPSQVAFASGSLLSPDPTTSPMSPSSSSASGHEDPLGIMGVNRRRSLL
                                                                          :*

E1-A0209P-8   PSFVLHVISPINWDVLR----RKPGCCLTKKNENTFDRRIAGVTFYRSQMMLVTVTGI
E1-A0209P-14   EGVSLDVPSHIDSKVRISPVPYLRLKKSRATKAQWVKEKGRLPFLTVYRAHMMLMTVICI
                .. *.* * *:.*   *   .   ** :   . *: :* **: :*** :** **

E1-A0209P-8   LAVDFTLFPRRYAKVETWGTSLMDLGVGSFMFSSGTVAGRKNDIKKPNAFKN------
E1-A0209P-14   LAVDFEVFPRWQGKCEDFGTSLMDVGVGSFVFSLGLVSTKSLSPPPPTPTPSSPALNSHI
                ***** :*** .* * :******:*****:** * *: :. . *:. .

E1-A0209P-8   --------------VLWNSFILLILGFARMFLTKSINYQEHVSEYGMHWNFFFTLGFMALG
E1-A0209P-14   IPLTPSPFTSILISLRKSIPILVLGFIRLIMVKGSDYPEHVTEYGVHWNFFFTLALVPVL
                * :*: :*:*** *::.*. :* ***:***:********. ::.:

E1-A0209P-8   VFFFRRSLKKVSYFNLATFITLLHHCLLVLTPFQKWALSAPRTNILAQNREGIASLPGYI
E1-A0209P-14   AVGIRPLTQWLRWSVLGVIISLLHQLWLTYY-LQSIVFSFGRSGIFLANKEGFSSLPGYL
                .. :* : : : : *..:*:***: *.   :* ..:* *:.*: *:**:*****:

E1-A0209P-8   AIYFYGMYTGSVVLADRP--------LMYTRAESWKRFQRLLFPLGILLVLYLVSNFLSV
E1-A0209P-14   SIFLIGLSIGDHVLRLSLPPRRERVVSETNEEHEQSHFERKKLDLIMELIGYSLGWWALL
                :*:: *: *. ** ,,, .. .:*:* :* : *: * :. : :

E1-A0209P-8   G-------VSRRLANTPYVANVAFINMFFLTIYILIDAYLFPSSVPYGSR---VPKLLE
E1-A0209P-14   GGWIWAGGEVSRRLANAPYVFWVAAYNTTFLLGYLLLTHIIPSPTSSQTSPSILVPPLLD
                *   ********:*** ** * ** *:*: :..:. *   ** **:

E1-A0209P-8   DANNNGLLVFLIANVLTGVVNLSFDTLHSSNAKGLTIMTMYLFIICYMAHWLAQHGIRFR
E1-A0209P-14   AMNKNGLAIFLAANLLTGLVNVSMKTMYAPAWLSMGVLMLYTLTISCVGWILKGRRIKI-
                *:*** :** **:***:**:*:.*::.. .: :: :* *. :. * : *::

E1-A0209P-8   L
E1-A0209P-14   -

query.dnd
(E1-A0209P-8:0.33007,E1-A0209P-14:0.33007);
</pre>